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1
SEQUENCE LISTING

<110> Guertler, Lutz G.
Eberle, Josef
Brunn, Albrecht V.
Knapp, Stefan
Hauser, Hans-Peter

<120> RETROVIRUS FROM HIV GROUP AND ITS USE

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<140> 09/109,916

<141> 1998-07-02

<150> DE P 42 33 646.5

<151> 1992-10-06

<150> DE P 42 35 718.7

<151> 1992-10-22

<150> DE P 42 44 541.8

<151> 1992-12-30

<150> DE P 43 18 186.4

<151> 1993-06-01

<160> 67

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<210> 34

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<223> Description of Artificial Sequence: primer

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<211> 20

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<223> Description of Artificial Sequence: primer

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<211> 20

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<223> Description of Artificial Sequence: primer

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 1 5 10 15
 ggt ata gtg caa cag cag gac aac ctg ctg aga gcg ata cag gcc cag 95
 Gly Ile Val Gln Gln Asp Asn Leu Leu Arg Ala Ile Gln Ala Gln
 20 25 30
 caa cac ttg ctg agg tta tct gta tgg ggt att aga caa ctc cga gct 143
 Gln His Leu Leu Arg Leu Ser Val Trp Gly Ile Arg Gln Leu Arg Ala
 35 40 45
 cgc ctg caa gcc tta gaa acc ctt ata cag aat cag caa cgc cta aac 191
 Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn
 50 55 60
 cta t 195
 Leu

<210> 38
 <211> 195
 <212> DNA
 <213> Human immunodeficiency virus

<400> 38
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 ctggtgcccgc tgcgc 195

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 <211> 64
 <212> PRT
 <213> Human immunodeficiency virus

<400> 39
 Ala Ala Ala Thr Ala Leu Thr Val Arg Thr His Ser Val Leu Lys Gly
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 Ile Val Gln Gln Gln Asp Asn Leu Leu Arg Ala Ile Gln Ala Gln Gln
 20 25 30
 His Leu Leu Arg Leu Ser Val Trp Gly Ile Arg Gln Leu Arg Ala Arg
 35 40 45

Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn Leu
 50 55 60

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<210> 41
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Met Ser Arg Pro Ile Ile Asn Ile His Thr Pro His Arg Glu Lys	
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aga cga gta gga ttg gga atg cta ttc ttg ggg gtg cta agt gca gca	95
Arg Arg Val Gly Leu Gly Met Leu Phe Leu Gly Val Leu Ser Ala Ala	
20 25 30	
ggt agc act atg ggc gca gcg gca aca gcg ctg acg gta cgg acc cac	143
Gly Ser Thr Met Gly Ala Ala Ala Thr Ala Leu Thr Val Arg Thr His	
35 40 45	
agt gta ctg aag ggt ata gtg caa cag cag gac aac ctg ctg aga gcg	191
Ser Val Leu Lys Gly Ile Val Gln Gln Asp Asn Leu Leu Arg Ala	
50 55 60	
ata cag gcc cag caa cac ttg ctg agg tta tct gta tgg ggt att aga	239
Ile Gln Ala Gln Gln His Leu Leu Arg Leu Ser Val Trp Gly Ile Arg	
65 70 75	
caa ctc cga gct cgc ctg caa gcc tta gaa acc ctt ata cag aat cag	287
Gln Leu Arg Ala Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln	
80 85 90 95	
caa cgc cta aac cta tgg ggc tgt aaa gga aaa cta atc tgt tac aca	335
Gln Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu Ile Cys Tyr Thr	
100 105 110	
tca gta aaa tgg aac aca tca tgg tca gga gga tat aat gat gac agt	383
Ser Val Lys Trp Asn Thr Ser Trp Ser Gly Gly Tyr Asn Asp Asp Ser	
115 120 125	
att tgg gac aac ctt aca tgg cag caa tgg gac caa cac ata aac aat	431
Ile Trp Asp Asn Leu Thr Trp Gln Gln Trp Asp Gln His Ile Asn Asn	
130 135 140	
gta agc tcc att ata tat gat gaa ata caa gca gca caa gac caa cag	479
Val Ser Ser Ile Ile Tyr Asp Glu Ile Gln Ala Ala Gln Asp Gln Gln	
145 150 155	
gaa aag aat gta aaa gca ttg ttg gag cta gat gaa tgg gcc tct ctt	527
Glu Lys Asn Val Lys Ala Leu Leu Glu Leu Asp Glu Trp Ala Ser Leu	
160 165 170 175	
tgg aat tgg ttt gac ata act aaa tgg ttg tgg tat ata aaa ata gct	575
Trp Asn Trp Phe Asp Ile Thr Lys Trp Leu Trp Tyr Ile Lys Ile Ala	
180 185 190	
ata atc ata gtg gga gca cta ata ggt ata aga gtt atc atg ata gta	623
Ile Ile Ile Val Gly Ala Leu Ile Gly Ile Arg Val Ile Met Ile Val	
195 200 205	

ctt aat cta gtg aag aac att agg cag gga tat caa ccc ctc tcg ttg 671
 Leu Asn Leu Val Lys Asn Ile Arg Gln Gly Tyr Gln Pro Leu Ser Leu
 210 215 220

cag atc cct gtc cca cac cgg cag gaa gca gaa acg cca gga aga aca 719
 Gln Ile Pro Val Pro His Arg Gln Glu Ala Glu Thr Pro Gly Arg Thr
 225 230 235

gga gaa gaa ggt gga gaa gga gac agg ccc aag tgg aca gcc ttg cca 767
 Gly Glu Glu Gly Gly Glu Gly Asp Arg Pro Lys Trp Thr Ala Leu Pro
 240 245 250 255

cca gga ttc ttg caa cag ttg tac acg gat ctc agg aca ata atc ttg 815
 Pro Gly Phe Leu Gln Gln Leu Tyr Thr Asp Leu Arg Thr Ile Ile Leu
 260 265 270

tgg act tac cac ctc ttg agc aac tta ata tca ggg atc cgg agg ctg 863
 Trp Thr Tyr His Leu Leu Ser Asn Leu Ile Ser Gly Ile Arg Arg Leu
 275 280 285

atc gac tac ctg gga ctg gga ctg tgg atc ctg gga caa aag aca att 911
 Ile Asp Tyr Leu Gly Leu Gly Leu Trp Ile Leu Gly Gln Lys Thr Ile
 290 295 300

gaa gct tgt aga ctt tgt gga gct gta atg caa tat tgg cta caa gaa 959
 Glu Ala Cys Arg Leu Cys Gly Ala Val Met Gln Tyr Trp Leu Gln Glu
 305 310 315

ttg aaa aat agt gct aca aac ctg ctt gat act att gca gtg tca gtt 1007
 Leu Lys Asn Ser Ala Thr Asn Leu Leu Asp Thr Ile Ala Val Ser Val
 320 325 330 335

gcc aat tgg act gac ggc atc atc tta ggt cta caa aga ata gga caa 1055
 Ala Asn Trp Thr Asp Gly Ile Ile Leu Gly Leu Gln Arg Ile Gly Gln
 340 345 350

gg 1057

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 acagctccac aaagtctaca agcttcaatt gtcttttgtc ccaggatcca cagtcccagt 180
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<400> 46

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Arg Val Gly Leu Gly Met Leu Phe Leu Gly Val Leu Ser Ala Ala Gly
 20 25 30

Ser Thr Met Gly Ala Ala Ala Thr Ala Leu Thr Val Arg Thr His Ser
 35 40 45

Val Leu Lys Gly Ile Val Gln Gln Gln Asp Asn Leu Leu Arg Ala Ile
 50 55 60

Gln Ala Gln Gln His Leu Leu Arg Leu Ser Val Trp Gly Ile Arg Gln
 65 70 75 80

Leu Arg Ala Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln
 85 90 95

Arg Leu Asn Leu Trp Gly Cys Lys Gly Lys Leu Ile Cys Tyr Thr Ser
 100 105 110

Val Lys Trp Asn Thr Ser Trp Ser Gly Gly Tyr Asn Asp Asp Ser Ile
 115 120 125

Trp Asp Asn Leu Thr Trp Gln Gln Trp Asp Gln His Ile Asn Asn Val
 130 135 140

Ser Ser Ile Ile Tyr Asp Glu Ile Gln Ala Ala Gln Asp Gln Gln Glu
 145 150 155 160
 Lys Asn Val Lys Ala Leu Leu Glu Leu Asp Glu Trp Ala Ser Leu Trp
 165 170 175
 Asn Trp Phe Asp Ile Thr Lys Trp Leu Trp Tyr Ile Lys Ile Ala Ile
 180 185 190
 Ile Ile Val Gly Ala Leu Ile Gly Ile Arg Val Ile Met Ile Val Leu
 195 200 205
 Asn Leu Val Lys Asn Ile Arg Gln Gly Tyr Gln Pro Leu Ser Leu Gln
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 Ile Pro Val Pro His Arg Gln Glu Ala Glu Thr Pro Gly Arg Thr Gly
 225 230 235 240
 Glu Glu Gly Gly Glu Gly Asp Arg Pro Lys Trp Thr Ala Leu Pro Pro
 245 250 255
 Gly Phe Leu Gln Gln Leu Tyr Thr Asp Leu Arg Thr Ile Ile Leu Trp
 260 265 270
 Thr Tyr His Leu Leu Ser Asn Leu Ile Ser Gly Ile Arg Arg Leu Ile
 275 280 285
 Asp Tyr Leu Gly Leu Gly Leu Trp Ile Leu Gly Gln Lys Thr Ile Glu
 290 295 300
 Ala Cys Arg Leu Cys Gly Ala Val Met Gln Tyr Trp Leu Gln Glu Leu
 305 310 315 320
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<211> 23

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<211> 21

<212> DNA

<213> Artificial Sequence

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<210> 52

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

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tccctaataaa attagcctgt c

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<210> 53

<211> 19

<212> DNA

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 aaacctccaa ttcccccta

19

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 <213> Human immunodeficiency virus

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 Cys Ile Arg Glu Gly Ile Ala Glu Val Gln Asp Ile Tyr Thr Gly Pro
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Met Arg Trp Arg Ser Met Thr Leu Lys Arg Ser Asn Asn Thr Ser Pro
 20 25 30

Arg Ser Arg Val Ala Tyr Cys
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<210> 55
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 <212> PRT
 <213> Human immunodeficiency virus

<400> 55
 Cys Ile Arg Glu Gly Ile Ala Glu Val Gln Asp Leu His Thr Gly Pro
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Leu Arg Trp Arg Ser Met Thr Leu Lys Lys Ser Ser Asn Ser His Thr
 20 25 30

Gln Pro Arg Ser Lys Val Ala Tyr Cys
 35 40

<210> 56
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 <212> DNA
 <213> Human immunodeficiency virus

<400> 56
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 <212> DNA
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<211> 1733

<212> DNA

<213> Human immunodeficiency virus

<400> 58

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<210> 59
 <211> 498
 <212> PRT
 <213> Human immunodeficiency virus

<400> 59
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 His Leu Val Trp Ala Ser Arg Glu Leu Glu Arg Tyr Ala Cys Asn Pro
 35 40 45
 Gly Leu Leu Glu Thr Ala Glu Gly Thr Glu Gln Leu Leu Gln Gln Leu
 50 55 60

Glu Pro Ala Leu Lys Thr Gly Ser Glu Asp Leu Lys Ser Leu Trp Asn
 65 70 75 80
 Ala Ile Ala Val Leu Trp Cys Val His Asn Arg Phe Asp Ile Arg Asp
 85 90 95
 Thr Gln Gln Ala Ile Gln Lys Leu Lys Glu Val Met Ala Ser Arg Lys
 100 105 110
 Ser Ala Glu Ala Ala Lys Glu Glu Thr Ser Pro Arg Gln Thr Ser Gln
 115 120 125
 Asn Tyr Pro Ile Val Thr Asn Ala Gln Gly Gln Met Val His Gln Ala
 130 135 140
 Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Ala Val Glu Glu Lys
 145 150 155 160
 Ala Phe Asn Pro Glu Ile Ile Pro Met Phe Met Ala Leu Ser Glu Gly
 165 170 175
 Ala Val Pro Tyr Asp Ile Asn Thr Met Leu Asn Ala Ile Gly Gly His
 180 185 190
 Gln Gly Ala Leu Gln Val Leu Lys Glu Val Ile Asn Glu Glu Ala Ala
 195 200 205
 Glu Trp Asp Arg Thr His Pro Pro Ala Met Gly Pro Leu Pro Pro Gly
 210 215 220
 Gln Ile Arg Glu Pro Thr Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr
 225 230 235 240
 Gln Gln Glu Gln Ile Ile Trp Thr Thr Arg Gly Ala Asn Ser Ile Pro
 245 250 255
 Val Gly Asp Ile Tyr Arg Lys Trp Ile Val Leu Gly Leu Asn Lys Met
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 Val Lys Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro
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 305 310 315 320
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 325 330 335
 Gly Pro Glu Ala Thr Leu Glu Glu Met Met Val Ala Cys Gln Gly Val
 340 345 350
 Gly Gly Pro Thr His Lys Ala Lys Ile Leu Ala Glu Ala Met Ala Ser
 355 360 365

Ala Gln Gln Asp Leu Lys Gly Gly Tyr Thr Ala Val Phe Met Gln Arg
370 375 380

Gly Gln Asn Pro Asn Arg Lys Gly Pro Ile Lys Cys Phe Asn Cys Gly
385 390 395 400

Lys Glu Gly His Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Arg Gly
405 410 415

Cys Trp Lys Cys Gly Gln Glu Gly His Gln Met Lys Asp Cys Lys Asn
420 425 430

Gly Arg Gln Ala Asn Phe Leu Gly Lys Tyr Trp Pro Pro Gly Gly Thr
435 440 445

Arg Pro Gly Asn Tyr Val Gln Lys Gln Val Ser Pro Ser Ala Pro Pro
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Asp Gln

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<211> 498

<212> PRT

<213> Human immunodeficiency virus

<400> 60

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Glu Arg Ile Arg Leu Arg Pro Gly Ser Lys Lys Ala Tyr Arg Leu Lys
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His Leu Val Trp Ala Ser Arg Glu Leu Glu Arg Tyr Ala Tyr Asn Pro
35 40 45

Gly Leu Leu Glu Thr Ala Glu Gly Thr Glu Gln Leu Leu Gln Gln Leu
50 55 60

Glu Pro Ala Leu Lys Thr Gly Ser Glu Asp Leu Lys Ser Leu Trp Asn
65 70 75 80

Ala Ile Ala Val Leu Trp Cys Val His Asn Arg Phe Asp Ile Arg Asp
85 90 95

Thr Gln Gln Ala Ile Gln Lys Leu Lys Glu Val Met Ala Ser Arg Lys
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Ser Ala Glu Ala Ala Lys Glu Glu Thr Ser Ser Thr Gln Ala Ser Gln
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Asn Tyr Pro Ile Val Thr Asn Ala Gln Gly Gln Met Val His Gln Ala
 130 135 140

Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Ala Val Glu Glu Lys
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 165 170 175

Ala Val Pro Tyr Asp Ile Asn Thr Met Leu Asn Ala Ile Gly Gly His
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Gln Gly Ala Leu Gln Val Leu Lys Glu Val Ile Asn Glu Glu Ala Ala
 195 200 205

Asp Trp Asp Arg Thr His Pro Pro Ala Met Gly Pro Leu Pro Pro Gly
 210 215 220

Gln Ile Arg Glu Pro Thr Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr
 225 230 235 240

Gln Gln Glu Gln Ile Ile Trp Thr Thr Arg Gly Ala Asn Ser Ile Pro
 245 250 255

Val Gly Asp Ile Tyr Arg Lys Trp Ile Val Leu Gly Leu Asn Lys Met
 260 265 270

Val Lys Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro
 275 280 285

Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg
 290 295 300

Ala Glu Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu
 305 310 315 320

Val Val Gln Asn Ser Asn Pro Asp Cys Lys Gln Ile Leu Lys Ala Leu
 325 330 335

Gly Pro Gly Ala Thr Leu Glu Glu Met Met Val Ala Cys Gln Gly Val
 340 345 350

Gly Gly Pro Thr His Lys Ala Lys Ile Leu Ala Glu Ala Met Ala Ser
 355 360 365

Ala Gln Gln Asp Leu Lys Gly Gly Tyr Thr Ala Val Phe Met Gln Arg
 370 375 380

Gly Gln Asn Pro Asn Arg Lys Gly Pro Ile Lys Cys Phe Asn Cys Gly
 385 390 395 400

Lys Glu Gly His Ile Ala Lys Asn Cys Arg Ala Pro Arg Arg Arg Gly
 405 410 415

Tyr Trp Lys Cys Gly Gln Glu Gly His Gln Met Lys Asp Cys Lys Asn
 420 425 430

Gly Arg Gln Ala Asn Phe Leu Gly Lys Tyr Trp Pro Pro Gly Gly Thr
 435 440 445

Arg Pro Ala Asn Tyr Val Gln Lys Gln Val Ser Pro Ser Ala Pro Pro
 450 455 460

Met Glu Glu Ala Val Lys Glu Gln Glu Asn Gln Asn Gln Lys Gly Asp
 465 470 475 480

Gln Glu Glu Leu Tyr Pro Phe Ala Ser Leu Lys Ser Leu Phe Gly Thr
 485 490 495

Asp Gln

<210> 61
 <211> 35
 <212> PRT
 <213> Human immunodeficiency virus type 1

<400> 61
 Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly
 1 5 10 15

Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Ala Val Pro Trp
 20 25 30

Asn Ala Ser
 35

<210> 62
 <211> 35
 <212> PRT
 <213> Human immunodeficiency virus

<400> 62
 Arg Leu Gln Ala Leu Glu Thr Leu Ile Gln Asn Gln Gln Arg Leu Asn
 1 5 10 15

Leu Trp Gly Cys Lys Gly Lys Leu Ile Cys Tyr Thr Ser Val Lys Trp
 20 25 30

Asn Thr Ser
 35

<210> 63
 <211> 25
 <212> PRT
 <213> Human immunodeficiency virus

<400> 63
 Trp Gly Ile Arg Gln Leu Arg Ala Arg Leu Gln Ala Leu Glu Thr Leu
 1 5 10 15

Ile Gln Asn Gln Gln Arg Leu Asn Leu
 20 25

<210> 64
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 64
 ccataatatt cagcagaact ag

22

<210> 65
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 65
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18

<210> 66
 <211> 36
 <212> PRT
 <213> Human immunodeficiency virus type 1

<400> 66
 Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Arg Ile Gln Arg
 1 5 10 15

Gly Pro Gly Arg Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg
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Gln Ala His Cys
 35

<210> 67
 <211> 36
 <212> PRT
 <213> Human immunodeficiency virus type 2

<400> 67
 Cys Lys Arg Pro Gly Asn Lys Ile Val Lys Gln Ile Met Leu Met Ser
 1 5 10 15

Gly His Val Phe His Ser His Tyr Gln Pro Ile Asn Lys Arg Pro Arg
 20 25 30

Gln Ala Trp Cys
 35